

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/752,639DATE: 01/31/2002
TIME: 04:08:58

INPUT SET: S36738.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

(1) General Information:

(i) APPLICANT: Gatanaga, T.
Granger, G.A.(ii) TITLE OF INVENTION: Factors Altering Tumor Necrosis
Factor Receptor Releasing Enzyme Activity, and Methods
of Use Thereof

(iii) NUMBER OF SEQUENCES: 154

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: MORRISON & FOERSTER

(B) STREET: 755 PAGE MILL ROAD

(C) CITY: Palo Alto

(D) STATE: CA

(E) COUNTRY: USA

(F) ZIP: 94304-1018

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette

(B) COMPUTER: IBM Compatible

(C) OPERATING SYSTEM: Windows

(D) SOFTWARE: FastSEQ for Windows Version 2.0b

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/752,639

(B) FILING DATE:

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PCT/US99/10793

(B) FILING DATE:

(A) APPLICATION NUMBER: 09/081,385

(B) FILING DATE:

(A) APPLICATION NUMBER: 08/964,747

(B) FILING DATE: 05-NOV-1997

(A) APPLICATION NUMBER: 60/030,761

(B) FILING DATE: 06-NOV-1996

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/752,639DATE: 01/31/2002
TIME: 04:08:58

INPUT SET: S36738.raw

47 (viii) ATTORNEY/AGENT INFORMATION:
48 (A) NAME: Wu, Frank
49 (B) REGISTRATION NUMBER: 41,386
50 (C) REFERENCE/DOCKET NUMBER: 22000-20577.21
51
52 (ix) TELECOMMUNICATION INFORMATION:
53 (A) TELEPHONE: 650-813-5600
54 (B) TELEFAX: 650-494-0792
55 (C) TELEX: 706141
56
57

58 (2) INFORMATION FOR SEQ ID NO:1:
59

60 (i) SEQUENCE CHARACTERISTICS:
61 (A) LENGTH: 4047 base pairs
62 (B) TYPE: nucleic acid
63 (C) STRANDEDNESS: double
64 (D) TOPOLOGY: linear
65
66 (ii) MOLECULE TYPE: Genomic DNA
67

68 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
69

70	AAGCTTTTTG	CTTTCCTTCC	CCGGGAAAGG	CCGGGGCCAG	AGACCCGCAC	TCGGACCAGG	60
71	CGGGGGCTGC	GGGGCCAGAG	TGGGCTGGGG	AGGGCTGGGA	GGGCGTCTGG	GGCCGGCTCC	120
72	TCCAGGCTGG	GGGCCGCCAG	CTCCGGGAAG	GCAGTCCTGG	CCTGCGGATG	GGGCCGCGCG	180
73	TGGGGCCCGG	CGGGGCGGCC	TCGGGAGGCG	TCCAGGCTGC	GGGAGCGGGA	GGAGCGGCCG	240
74	TGCGGGCGCC	AGCGCCGTGG	GTGGAGGTGC	CCGTCCCTCC	TGAGGGGCAG	CCAGTGCGTT	300
75	TGGGACCCGG	GAGCAGAGCC	CGCGCCTCCC	CAGCGGCCTC	CCCGGGGGTC	TCACCGGGTC	360
76	ACCCGAGAGC	GGAGGCCCCG	GCTCCGCAGA	AACCCGGGGC	GGCCGCGGGG	AAGCAGCGCC	420
77	CTCAGGCGTC	GGAGGAGCCC	CCAGAAGGAC	CTCGCGCCTT	CCCGCCGGGC	TCCGACCGCC	480
78	TGGGTTCCGT	GCGGGACGGC	CCAGGCCGCC	AGGACCCCA	AGCGCAGCTC	AGTCTGCGGG	540
79	GCACGACCCA	GAGGCCAGCA	GAGGCCAGCA	GGGCCGGGGC	CGGGAGAGGG	CGGGAGGGGC	600
80	GCTCCTGGGA	GGTCAAGGCC	AGGGCTAGAC	TTTCAGGGTC	ATGGCCTGGC	CCCTCATCCC	660
81	CAGGGAGGTG	AGGGGGCTCT	GTGAGCAGAG	GGGGCCCCGG	TGGAGAAGGC	GCTGCTAGCC	720
82	AGGGGCGGGG	CAGGAGCCCA	GGTGGGGACT	TAAGGGTGGC	TGAAGGGACC	CTCAGGCTGC	780
83	AGGGATAGGG	AGGGAAGCTA	GGGGTGTGGC	TTGGGGAGGT	GCTGGGGGAC	CGCGGGCGCC	840
84	CTTTATTCTG	AAGCCGAATG	TGCTGCCGGA	GTCCCCAGTG	ACCTAGAAAT	CCATTTCAG	900
85	ATTTTCAGGA	GTTTCAGGTG	GAGACAAAGG	CCAGGCCCCAG	GTGAAAATGT	GGCAGTGACA	960
86	GAGTATGGGG	TGAGAACCAC	GGAGAGAGGA	AGTCCCCGAG	GCGGATGATG	GGACAGAGAG	1020
87	CGGGGACCAG	AATTTTTTAA	AACGCATCTG	AGATGCGTTT	GGCAGACTCA	TAGTTGTTTT	1080
88	CCTTTCACGG	AGAAAGTGTG	GGCAGAAGCC	AGCTCTAAAG	CCCAGGCTGC	CCAGCCTGCA	1140
89	CTGGCAGAGC	TGACGGAAGG	CCAGGGCAGA	GCCTTCCCTC	CCTGTCACAG	ACATGAGCCC	1200
90	TGGAGATCTG	GAATGAGGCA	GATGTGCCCA	GGGAAAGCTG	ATCCGCCCCG	ACCCAGGGCC	1260
91	CCCCGGGTGC	CCCTTTGAGC	GTGGAATCGT	TGCCAGGTCA	TGGCTCCCTG	CTATCGAACA	1320
92	CCGGACACGG	GTCGTGTGCT	GCACCTGGCA	GTTGCAGGAC	CGACACCCAC	AATGCCTTAA	1380
93	GAGGTGATGA	CTGCCTTCCA	GGGGCCTGGC	TGGCTGACAC	TTTGCATGGC	TCCTGGAGAA	1440
94	GAGGGATTGA	GTGGAGTCCA	CGGGTCATGG	CCACGTCCTG	GGTGCTGCCT	CTGAGGCAGG	1500
95	GCCCCGGCTG	GGTGAGAAGG	GGCTGGAGAC	AGGTTCTCTG	CAGTTCAGCC	TCTAACCGGT	1560
96	GGTCTTCATG	CCTAGGAACC	CACTGGGGGC	TTATGAAACT	GCAGGTGGCT	GAGTCCTTGC	1620
97	CATGGGGTCT	CTCCTTCAGG	AGGTCTGGGT	GGGGCCGGAG	ACTGTACCCC	ACAAAGGGTC	1680
98	CCAGGTGAGG	CGGATGTGGC	CTGGCGCTGT	GTGGCTCTGG	ACCTAGTCCT	TGGGCTTGGG	1740
99	CTGGCGCCCA	GGGCTGGGC	TTGAGACAGC	TGTGACGCAG	GCAAGCCATT	TACCCCGTTT	1800

RAW SEQUENCE LISTING PATENT APPLICATION US/09/752,639

DATE: 01/31/2002
TIME: 04:08:59

INPUT SET: S36738.raw

100	GTGGGGACAT	TACATCTTCC	TAGCTTGGAA	CACACAGGCA	GCCAGGGTTG	TTATCCACAT	1860
101	TCCTCCTCCA	TGTTCTTCTC	TTGAGAACTT	TTACCAGGTA	TGTCAGGAGC	TGGGCTCCAC	1920
102	CAGGGAGACT	CAAGTGGA	GCCCTCATCC	TTGTCTCCA	GGAGACAGGA	AAACCTATGG	1980
103	TTACAATTCC	AGGGACAAGA	GCGATGCATG	TGAGGTGTGG	CAAATCTCAC	TGTTCAACTG	2040
104	GAGAAATCAG	AGACAGCTTC	CTGGAGGCAG	TGACACCTGG	ACAGGCTTCT	CCACAGGAGG	2100
105	AAGCGAGTGA	GAGAAGCCAA	CTGGGATGGA	CCCATCATGT	AGGGGGAACA	GTGCGCGCAG	2160
106	AACCAACAAC	CACCCCCACC	CTAGGCCAG	AGCTCACGGA	GAGAGCTGGG	CCTCTCGGGG	2220
107	TGACTACATA	GTTCCCTGCT	GGATCTTAGG	TCTTGTCCTT	GGGCAGCTCT	GCTGAGACCT	2280
108	CTATGCCTGT	TCCAGGCTGC	ACCAAGGTTT	TGTGACTATT	GGTCTGGGGT	TGTTTTGCAG	2340
109	CAACTGAAGT	GTTCTGTTGT	AAAACAGGCA	CTTGATTTGC	TGGAAGGAAT	GCTGTTTGTT	2400
110	CTTGCTGCGA	CAAACATTGA	GCAGCATTTA	GTGGGCGGTT	TATATCTTGT	GGAGTAATGG	2460
111	GTGTTTTTGA	AGTCTGTCCT	GGGTACTGCA	CATTAAGG	AATATCATTT	TCTGAAACAT	2520
112	TGCTATTTTC	CACACCAGAA	ATCATATCCT	CCTGCTGGTC	CATGTCTGAA	GACCTTACAC	2580
113	GAGAAAGTCT	TAATGTAAGT	TTAGTAGAGT	CCTTGGATGG	AGAACTAATT	ATATCATACA	2640
114	TTGCCGCTTT	CTCACTCTGC	TCTTTTTTCAT	CCTTGCCTAA	TTTCATTTTC	TTCTGCTTCT	2700
115	TTTGTTTTCT	TTCTGGAGAA	TCTAGCAAGA	TATCTGGTGG	AACATCTCGA	GGTGATGAAC	2760
116	AAGGTAGAGA	CTGAGATTGT	AGGATTAAAG	GTGGTCTTGA	GCCTTTAGGA	GTTCTTTCAC	2820
117	TTCCAGCAGG	GGAGCATACT	GGCTGTGGAG	ATCTCAAGGG	AAAAGATGCA	GCATTCTCA	2880
118	TTGTTGAAGA	ATCTCCATCG	TCACTACTTA	GCCTGTGCAC	CATGTGTAGG	TAGTCTCAC	2940
119	TTGAACCATG	TCTAGGATTA	TCAGCATGAT	GATTAGCTGA	ATTGCCAGAC	AACGGACCAG	3000
120	AAACTTTATT	ATCATGTATG	TTTCTCAAAC	CACCTGCAAC	AATGGGACTT	GATACCGATG	3060
121	CTTGTTGCAT	CTGTGGATGT	GTTGTGTAAC	TTGAAGGATG	GGAATATGGC	ATGTATCCTG	3120
122	CAGGGCTTTG	TGGGGCGTAT	GGACTAGGCA	CTGGGCTATT	TTGCTGTGGC	ATAAATCTGT	3180
123	TCCCAGAGCT	TGTCTGTGGT	GGCACAACC	GGCTGGAGGG	GCTATGTGAG	ATAGTGGTTT	3240
124	GTTGATAATT	GGAAGATGCA	GGACTACTGT	GCATGGAATT	CTGAGAAAGT	TTATACTGAG	3300
125	ACATCATCAT	TCCACTTTGT	ACATATCTGT	TCTGCATGCT	TTTCTCCCTG	AAAACATTAG	3360
126	GACTCCTTGC	CAGGACGGCC	TGCAACAAGA	CTGGTATGTC	ACCTTCTGGG	TCATCACTGC	3420
127	CAAGGTTATC	TTTCAACTCT	ATGTGATCTG	TTGATACCTG	GTTGAGGCTA	TGGACAAGCT	3480
128	GTGAAACCAA	ATTGTCATCC	CTACAAGCCA	AAAGGCAGTT	CACCTCTTCT	GCTATTTCGTG	3540
129	CATTAAAGAG	AAGGCTCTTT	GTAGTTGTAG	CAGGTAAAGG	AGATGGAAGA	GGCAGCTGGT	3600
130	TCAGGAGGTC	TGTGAGACTA	GCAATCCCCG	CAAGAGTAGT	AATGGGGACA	TGGGGCATAT	3660
131	CCCCATTCAT	CCTGAATTTT	TGGAATGGTG	TTGCCTATAA	AAGTACTTAG	TTCAGGTGCC	3720
132	AGCTGTCAAT	ACTTCCCATT	TCCCAAACAC	TGGGCGAATC	GGCGTCTGAA	TCCAAGGGGA	3780
133	GGCCGAGGCC	GCTGTGGCGA	GAGACTATAA	TCCGGGCCGG	GAGGGGGGGC	GGCTACGGCT	3840
134	CCTCTTCCGT	CTCCTCAGTG	CGGGGAACAT	GTAGAGCCGG	GGGGAGACCA	GCCGAGAAGA	3900
135	CAAATCGTTG	CTTCTTCTTC	CTCCTCTCC	TCCTTCTCCC	ACATAGAAAC	ACTCACAAC	3960
136	ACCCGACCAC	GGGCCCAGC	TACCGGGGGG	GCATCGCCGC	GGGCCCAGGA	ACCAATTCTC	4020
137	CTGTCGGCGG	GGGCGTCCTT	TGGATCC				4047

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 739 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

151	GGATCCAAAG	GTCAAACCTCC	CCACCTGGCA	CTGTCCCCGG	AGCGGGTCGC	GCCCCGGCCG	60
152	CGCGCGGCCG	GGCGCTTGGC	GCCAGAAGCG	AGAGCCCCCTC	GGGGCTCGCC	CCCCGCCTC	120

RAW SEQUENCE LISTING PATENT APPLICATION US/09/752,639

DATE: 01/31/2002
TIME: 04:08:59

INPUT SET: S36738.raw

153	ACCGGGTCAG	TGAAAAACG	ATCAGAGTAG	TGGTATTTCA	CCGGCGGGCC	GCAGGGCCCG	180
154	CGGACCCCGC	CCCGGGCCCC	TCGCGGGGAC	ACCGGGGGGG	CGCCGGGGGC	CTCCCACTTA	240
155	TTCTACACCT	CTCATGTCTC	TTCACCGTGC	CAGACTAGAG	TCAAGCTCAA	CAGGGTCTTC	300
156	TTTCCCGCT	GATTCCGCCA	AGCCCGTTCC	CTTGGCTGTG	GTTTCGCTGG	ATAGTAGGTA	360
157	GGGACAGTGG	GAATCTCGTT	CATCCATTCA	TGCGCGTCAC	TAATTAGATG	ACGAGGCATT	420
158	TGGCTACCTT	AAGAGAGTCA	TAGTTACTCC	CGCCGTTTAC	CCGCGCTTCA	TTGAATTCT	480
159	TCACTTTGAC	ATTGAGAGCA	CTGGGCAGAA	ATCACATCGC	GTCAACACCC	GCCGCGGGCC	540
160	TTCGCGATGC	TTTGTTTTAA	TTAAACAGTC	GGATTCCCCT	GGTCCGCACC	AGTTCTAAGT	600
161	CGGCTGCTAG	GCGCCGGCCG	AAGCGAGGCG	CCGCGCGGAA	CCGCGGCCCC	CGGGGCGGAC	660
162	CCGCGGGGGG	GACCGGGCCG	CGGCCCCTCC	GCCGCCTGCC	GCCGCCCGCG	CCGCCGCGCG	720
163	CCGAAGAAGA	AGGGGGAAA					739

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 233 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

177	CAAGAGTGGC	GGCCGCAGCA	GGCCCCCGG	GTGCCCGGGC	CCCCCTCGAG	GGGGACAGTG	60
178	CCCCCGCCGC	GGGGGCCCG	CGGCGGGCCG	CCGCCGGCCC	CTGCCGCCCC	GACCCCTTCTC	120
179	CCCCCGCCGC	CGCCCCACG	CGGCGCTCCC	CCGGGGAGGG	GGGAGGACGG	GGAGCGGGGG	180
180	AGAGAGAGAG	AGAGAGAGGG	CGCGGGGTGG	CTCGTGCCGA	ATTCAAAAAG	CTT	233

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2998 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

194	GGATCCAAAG	AATTCGGCAC	GAGGTAGTCA	CGGCTCTTGT	CATTGTTGTA	CTTGACGTTG	60
195	AGGCTGGTGA	GCTTGGAAAA	GTGATGCGC	AGCGTGACG	AGGCGTTGTA	GATGTTCTGC	120
196	CCGTCCAGCG	ACAGCTTGGC	GTGCTGGGCG	CTCACGGGGT	CCGCATACTG	CAGCAGGGCC	180
197	TGGAACCTGGT	TGTTCTTGGT	GAAGGTGATG	ATCTTCAACA	CTGTGCCGAA	CTTGGAGAAA	240
198	ATCTGGTGCA	GCACATCCAG	GGTCACAGGG	TAGAAGAGGT	TCTCCACGAT	GATCCTGAGC	300
199	ACGGGGCTCT	GCCCGGCCAT	CGCCATCCCT	GCATCCACGG	CCGCCGCCGA	GGCAGCCAAG	360
200	GCCAGGTTCC	CCGACTGGAC	CGAGTTCACC	GCCTGCAGGG	CCGCCTGGGC	CCGCGCCTGG	420
201	TTGGGAGAGC	TGTCGGTCTT	CAGCTCCTTG	TGGTTGGAGA	ACTGGATGTA	GATGGGCTGG	480
202	CCGCGCAGCA	CAGGGGTCAC	CGAGGTGTAG	TAGTTACCA	TGGTATTGGC	AGCCTCCTCC	540
203	GTGTTTCATCT	CGATGAAGGC	CTGGTTTTTC	CCCTTCAGCA	TCAGGAGGTT	GGTGACCTTC	600
204	CCAAAGGGCA	GCCCCAGGGA	GATGACTTCC	CCCTCCGTGA	CGTCGATGGG	GAGCTTCCGG	660
205	ATGTGGATCA	CTCTAGAGGG	GACGCCTGCA	CTTCGGCTGT	CACCTTTGAA	CTTCTTGCTG	720

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/752,639DATE: 01/31/2002
TIME: 04:08:59

INPUT SET: S36738.raw

206	TCATTTCCGT	TTGCTGCAGA	AGCCGAGTTG	CTGCTCATGA	TAAACGGTCC	GTTAGTGACA	780
207	CAAGTAGAGA	AAAGCTCGTC	AGATCCCCGC	TTTGTACCAA	CGGCTATATC	TGGGACAATG	840
208	CCGTCCATGG	CACACAGAGC	AGACCCGCGG	GGGACGGAGT	GGAGGCGCCG	GAATCCTGGA	900
209	GCTAGAGCTG	CAGATTGAGT	TGCTGCGTGA	GACGAAGCGC	AAGTATGAGA	GTGTCCCTGCA	960
210	GCTGGGCCGG	GCACTGACAG	CCCACCTCTA	CAGCCTGCTG	CAGACCCAGC	ATGCACTGGG	1020
211	TGATGCCTTT	GCTGACCTCA	GCCAGAAGTC	CCCAGAGCTT	CAGGAGGAAT	TTGGCTACAA	1080
212	TGCAGAGACA	CAGAAACTAC	TATGCAAGAA	TGGGGAAACG	CTGCTAGGAG	CCGTGAACCT	1140
213	CTTTGTCTCT	AGCATCAACA	CATTGGTCAC	CAAGACCATG	GAAGACACGC	TCATGACTGT	1200
214	GAAACAGTAT	GAGGCTGCCA	GGCTGGAATA	TGATGCCTAC	CGAACAGACT	TAGAGGAGCT	1260
215	GAGTCTAGGC	CCCCGGGATG	CAGGGACACG	TGGTCGACTT	GAGAGTGCCC	AGGCCACTTT	1320
216	CCAGGCCCAT	CGGGACAAGT	ATGAGAAGCT	GCGGGGAGAT	GTGGCCATCA	AGCTCAAGTT	1380
217	CCTGGAAGAA	AACAAGATCA	AGGTGATGCA	CAAGCAGCTG	CTGCTCTTCC	ACAATGCTGT	1440
218	GTCGCGCTAC	TTTGCTGGGA	ACCAGAAACA	GCTGGAGCAG	ACCCTGCAGC	AGTTCAACAT	1500
219	CAAGCTGCGG	CCTCCAGGAG	CTGAGAAACC	CTCCTGGCTA	GAGGAGCAGT	GAGCTGCTCC	1560
220	CAGCCCAACT	TGGCTATCAA	GAAAGACATT	GGGAAGGGCA	GCCCCAGGGT	GTGGGAGATT	1620
221	GGACATGGTA	CATCCTTTGT	CACTTGCCCT	CTGGCTTGGG	CTCCTTTTTC	TGGCTGGGGC	1680
222	CTGACACCAG	TTTTGCCAC	ATTGCTATGG	TGGGAAGAGG	GCCTGGAGGC	CCAGAAGTTG	1740
223	CTGCCCTGTC	TATCTTCCTG	GCCACAGGGC	TTCATTCCCA	GATCTTTTCC	TTCCACTTCA	1800
224	CAGCCAACGG	CTATGACAAA	ACCACTCCCT	GGCCAATGGC	ATCACTCTTC	AGGCTGGGGT	1860
225	GTGCTCCCTG	ACCAATGACA	GAGCCTGAAA	ATGCCCTGTC	AGCCAATGGC	AGCTCTTCTC	1920
226	GGACTCCCTT	GGGCCAATGA	TGTTGCGTCT	AATACCCCTT	GTCTCTCCTC	TATGCGTGCC	1980
227	CATTGCAGAG	AAGGGGACTG	GGACCAAAGG	GGTGGGGATA	ATGGGGAGCC	CCATTGCTGG	2040
228	CCTTGCACTT	GAATAGGCCT	ACCCTCACCA	TTTATTCACT	AATACATTTT	ATTGTGTTC	2100
229	TCTAATTTAA	AATTACCTTT	TCATCTTGCT	TGATTTTCCT	TCAGCTAAAT	TAGAAATTTG	2160
230	TAGTTTTTCC	CCTAAAAAAT	TCAATGGCAT	TCTTTCTTAT	AAATTACATT	CTCTGATTTT	2220
231	CTTGTCAGCC	TGCTTCAAGG	AAATCCATGT	GTTCAAAAATG	CTTGCTCGCA	GTTTGCTCCA	2280
232	TACCAAATGG	TTGCTTAACC	CAAATATCTG	AGCAGCAAAT	TGAGCTGATC	CTTCTGGAGA	2340
233	AAGTACGGTT	GAACAGCCAA	GACCACTGGG	TAGTCGAAGA	GAAGACCACA	CATCCTGAAC	2400
234	TCCCCAGTCT	GGTGTGAGGG	GAGGACAGCT	GATAACTGGA	TATGCAGTGT	TCCCAGACAT	2460
235	CACTGGTCCC	AAACCATTAC	TTCTGCCTGC	CACTGCCACA	AATACAGTAG	GAATGCCATC	2520
236	CCCTTCATAC	TCAGCTTTAA	TCCTCAGAGT	TTCATCTGGT	CCTTTATGCG	CAGATGTTAC	2580
237	TCGAAGTTCA	CATGGAATGC	CAAAATTTCC	ACAGGCCTTC	TTGATTTTTT	CACAGTGACC	2640
238	AAGATCAGAA	GTAGAGCCCA	TCAACACTAC	AACCCCTGCAC	TGACTTTCTG	ATTTCAAAG	2700
239	CAACTCTACT	CTCTCTGCAA	CCCCTCAAAA	GTTTTTCTTT	ACCATTGGA	GCCCTTCAGG	2760
240	AGTTACTTCT	TTGAGGTCCC	GATAAGACTG	TTTGTCTTTC	TGTTGGCTTC	GATCTCCTGA	2820
241	TGGCCAGAGT	CTCCAGGAAT	CATTGTCAAT	AACATCAGCA	AGAACAATTT	CTTTGGTGGT	2880
242	TACATCAACA	CCAAATTCAA	TCTTCATATC	AACCAGTGTA	CAATTCTGGG	GCAACCAGGA	2940
243	TTTCTCCAGT	ATTTCAAATA	TAGCCTGTGT	AGCATCTCGT	GCCGAATTCA	AAAAGCTT	2998

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4152 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

257	AAGCTTTTTG	TGAAAACCCCT	AGGATATGTC	CCCTCCCTCA	CCACACCCAA	CCCCCGCCCC	60
258	CTGCCCCAGG	ACATGACGAT	GCCTCACACA	CACACACACA	CACACATACA	CACAAGGCCG	120

PAGE: 1

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/09/752,639

DATE: 01/31/2002
TIME: 04:09:00

INPUT SET: S36738.raw

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Original Text